Sub Bundle

dehydrogenase], integrated into the chromosome, under conditions suitable for production of polyhydroxybutyrate-polyhydroxyvalerate by the transgenic organism.

1. (clean copy of amended claim) A method for the biological production of polyhydroxyalkanoate containing 3-hydroxyhexanoate comprising growing a transgenic organism selected from the group consisting of a transgenic bacterium and a transgenic plant having at least one bacterial transgene encoding an enzyme selected from the group consisting of a PHA polymerase incorporating C_6 substrates and a D-specific enoyl-CoA hydratase, integrated into the chromosome, under conditions suitable for production of polyhydroxybutyrate-polyhydroxyvalerate by the transgenic organism.

C1 cont'd.

2. (amended) The method of claim 1 wherein the organism is a [bacteria or] plant.

2. (clean copy of amended claim) The method of claim 1 wherein the organism is a plant.

3. (amended) The method of claim 2 wherein the organism is a plant selected from the group consisting of an oil crop [plants] plant and a starch accumulating [plants] plant.

3. (clean copy of amended) The method of claim 2 wherein the organism is a plant selected from the group consisting of an oil crop plant and a starch accumulating plant.

4. (amended) The method of claim 3 wherein the plant is selected from the group consisting of [Brassica] *Brassica*, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.

4. (clean copy of amended claim) The method of claim 3 wherein the plant is selected from the group consisting of *Brassica*, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.

C1 concld.

5. (amended) The method of claim [2] 1 wherein the organism is a [bacteria] bacterium selected from the group consisting of *Escherichia, Klebsiella, Ralstonia, Alcaligenes, Pseudomonas,* and *Azotobacter*.

5. (clean copy of amended claim) The method of claim 1 wherein the organism is a bacterium selected from the group consisting of *Escherichia, Klebsiella, Ralstonia, Alcaligenes, Pseudomonas,* and *Azotobacter*.

7. (amended) The method of claim 6 wherein the [enzyme] polymerase is [derived] from *Aeromonas caviae, Comamonas testosteroni, Thiocapsia pfenigii, Chromatium vinosum, Bacillus cereus, Nocardia carolina, Nocardia salmonicolor, Rhodococcus ruber, Rhodcoccus rhodocrous,* and *Rhodospirilum rubrum*.

C2

7. (clean copy of amended claim) The method of claim 6 wherein the polymerase is from *Aeromonas caviae, Comamonas testosteroni, Thiocapsia pfenigii, Chromatium vinosum, Bacillus cereus, Nocardia carolina, Nocardia salmonicolor, Rhodococcus ruber, Rhodcoccus rhodocrous,* and *Rhodospirilum rubrum*.

Sub E4

8. (amended) The method of claim 1 wherein the [organisms are] organism is genetically engineered to redirect metabolites to production of 3-hydroxyhexanoyl-CoA.

8. (clean copy of amended claim) The method of claim 1 wherein the organism is genetically engineered to redirect metabolites to production of 3-hydroxyhexanoyl-CoA.

Sub E5

9. (amended) The method of claim 8 wherein the [organisms are] organism is genetically engineered using a D-specific enoyl-CoA hydratase gene.

9. (clean copy of amended claim) The method of claim 8 wherein the organism is genetically engineered using a D-specific enoyl-CoA hydratase gene.

10. (amended) The method of 9 wherein the hydratase gene is isolated from a [bacteria] bacterium selected from the group consisting of *R. eutropha, Klebsiella aerogenes, P. putida,* and *Aeromonas caviae.*

10. (clean copy of amended claim) The method of 9 wherein ~~the~~ hydratase gene is isolated from a bacterium selected from ~~the group~~ consisting of *R. eutropha, Klebsiella aerogenes, P. putida, and Aeromonas caviae.*

11. (amended) The method of claim 8 wherein the [organisms are] organism is genetically engineered using the genes encoding the enzymes in a butyrate fermentation pathway.

11. (clean copy of amended claim) The method of claim 8 wherein the organism is genetically engineered using the genes encoding the enzymes in a butyrate fermentation pathway.

12. (amended) The method of claim 11 wherein the enzymes in the butyrate fermentation pathway [is] are from *Clostridium acetobutylicium* or *Thermoanaerobacterium thermosaccharolyticum.*

12. (clean copy of amended claim) The method of claim 11 wherein the enzymes in the butyrate fermentation pathway are from *Clostridium acetobutylicium* or *Thermoanaerobacterium thermosaccharolyticum.*

13. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to convert butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.

13. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to convert butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.

14. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a broad range reductase that is active on C_6 substrates.

14. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a broad range reductase that is active on C_6 substrates.

15. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a polymerase that accepts 3-hydroxyhexanoyl CoA.

15. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a polymerase that accepts 3-hydroxyhexanoyl CoA.

16. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express a thiolase accepting acetoacetyl CoA.

16. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express a thiolase accepting acetoacetyl CoA.

17. (amended) The method of claim 11 wherein the [organisms are] organism is genetically engineered to express an enzyme selected from the group consisting of thiolases specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, [PHA polymerase that accepts 3-hydroxybutyryl CoA] and 3-hydroxyhexanoyl CoA.

17. (clean copy of amended claim) The method of claim 11 wherein the organism is genetically engineered to express an enzyme selected from the group consisting of thiolases

specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, and 3-hydroxyhexanoyl CoA.]

18. (amended) The method of claim 8 wherein the [organisms are] organism is further genetically engineered [using] to express one or more fatty acid biosynthetic enzymes.

18. (clean copy of amended claim) The method of claim 8 wherein the organism is further genetically engineered to express one or more fatty acid biosynthetic enzymes.

22. (amended) The method of claim 18 wherein the enzymes are [derived] from *E. coli*.

[22. (clean copy of amended claim) The method of claim 18 wherein the enzymes are from *E. coli*.]

23. (amended) The method of claim 8 wherein the [organisms are] organism is further genetically engineered [using a] to express one or more enzymes forming a fatty acid oxidation complex.

23. (clean copy of amended claim) The method of claim 8 wherein the organism is further genetically engineered to express one or more enzymes forming a fatty acid oxidation complex.

25. (amended) The method of claim 24 wherein the enzymes are [derived] from *Nocardia salmonicolor*.

[25. (clean copy of amended claim) The method of claim 24 wherein the enzymes are from *Nocardia salmonicolor*.]

26. (amended) The method of claim 24 wherein the epimerizing enzymes [for epimerization] are [derived] from the *Pseudomonas putida* FaoAB complex.